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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/035,060C

DATE: 03/13/2003

TIME: 14:19:22

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\03132003\J035060C.raw

3 <110> APPLICANT: Edwards, David L.
 4 Hernstadt, Corinna
 5 Wilcox, Edward R.
 6 Wong, Siu-Yin
 8 <120> TITLE OF INVENTION: Process for Altering the Host Range of *Bacillus thuringiensis* Toxins, and
 9 Novel Toxins Produced Thereby
 11 <130> FILE REFERENCE: M12C1FDF3D2
 13 <140> CURRENT APPLICATION NUMBER: US 10/035,060C
 14 <141> CURRENT FILING DATE: 2001-12-27
 16 <150> PRIOR APPLICATION NUMBER: US 09/405,788
 17 <151> PRIOR FILING DATE: 1999-09-27
 19 <150> PRIOR APPLICATION NUMBER: US 08/855,160
 20 <151> PRIOR FILING DATE: 1997-05-13
 22 <150> PRIOR APPLICATION NUMBER: US 08/580,781
 23 <151> PRIOR FILING DATE: 1995-12-29
 25 <150> PRIOR APPLICATION NUMBER: US 08/420,615
 26 <151> PRIOR FILING DATE: 1995-04-10
 28 <150> PRIOR APPLICATION NUMBER: US 08/097,808
 29 <151> PRIOR FILING DATE: 1993-07-27
 31 <150> PRIOR APPLICATION NUMBER: US 07/980,128
 32 <151> PRIOR FILING DATE: 1992-11-23
 34 <150> PRIOR APPLICATION NUMBER: US 07/803,920
 35 <151> PRIOR FILING DATE: 1991-12-06
 37 <150> PRIOR APPLICATION NUMBER: US 07/356,599
 38 <151> PRIOR FILING DATE: 1989-05-24
 40 <150> PRIOR APPLICATION NUMBER: US 06/904,572
 41 <151> PRIOR FILING DATE: 1986-09-05
 43 <150> PRIOR APPLICATION NUMBER: US 06/808,129
 44 <151> PRIOR FILING DATE: 1985-12-12
 46 <160> NUMBER OF SEQ ID NOS: 9
 48 <170> SOFTWARE: PatentIn version 3.1
 50 <210> SEQ ID NO: 1
 51 <211> LENGTH: 3531
 52 <212> TYPE: DNA
 53 <213> ORGANISM: *Bacillus thuringiensis*
 55 <400> SEQUENCE: 1

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60 tcgctaacgc aatttctttt gagtgaattt gttcccggtg ctggatttgt gttaggacta	180
62 gttgatataa tatggggaat ttttgttccc tctcaatggg acgcatttct tgtacaaatt	240
64 gaacagttaa ttaacccaaag aatagaagaa ttgcgttagga accaagccat ttcttagatta	300
66 gaaggactaa gcaatctta tcaaatttac gcagaatctt ttagagatgt ggaagcagat	360
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74	aggtggggat	ttgatgccgc	gactatcaat	agtcgttata	atgatttAAC	taggcttatt	600
76	ggcaactata	cagattatgc	tgtacgctgg	tacaatacgg	gattagaacg	tgtatgggaa	660
78	ccggattcta	gagattgggt	aaggtaataat	caatttagaa	gagaattaac	actaactgtt	720
80	ttagatatcg	ttgctctgtt	cccgaaattat	gatagttagaa	gataatccaat	tcgaacagtt	780
82	tcccaattaa	caagagaaat	ttatacAAC	ccagtattag	aaaatttga	tggtagttt	840
84	cgaggctcgg	ctcaggcat	agaaaagaagt	attaggagtc	cacatttgc	ggatatactt	900
86	aacagtataa	ccatctatac	ggatgctcat	aggggttatt	attattggc	agggcatcaa	960
88	ataatggctt	ctcctgtagg	gttttcgggg	ccagaattca	cttttccgct	atatggaaact	1020
90	atgggaaatg	cagctccaca	acaacgtatt	gttgctcaac	tagtcaggg	cgtgtataga	1080
92	acattatcgt	ccacttata	tagaagacct	tttaatata	ggataaataa	tcaacaacta	1140
94	tctgttcttg	acgggacaga	atttgcttat	ggaacctcct	caaatttgc	atccgctgt	1200
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122	ctggatgaaa	aacaagaatt	gtccgagaaa	gtcaaacatg	cgaagcgact	tagtgcgt	2040
124	cggaaatttac	ttcaagatcc	aaacttcaga	gggatcaata	gacaactaga	ccgtggctgg	2100
126	agaggaagta	cggatattac	catccaagga	ggcgatgacg	tattcaaaga	gaattacgtt	2160
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156	caaaacaacc	aacgttcgg	ccttgcTTT	ccggaatggg	aagcagaatgt	gtcacaagaa	3060
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162	aactgcgtag	aagaggaaat	ctatccaaat	aacacggtaa	cgtgtatga	ttatactgt	3240
164	aatcaagaag	aataccggagg	tgcgtacact	tctcgtaatc	gaggatataa	cgaagctcct	3300
166	tccgtaccag	ctgattatgc	gtcagtctat	gaagaaaaat	cgtatacaga	tggacgaaga	3360

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 170 gtgacaaaag aattagaata cttccagaa accgataagg tatggattga gattggagaa 3480
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 175 <210> SEQ ID NO: 2
 176 <211> LENGTH: 1177
 177 <212> TYPE: PRT
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 180 <400> SEQUENCE: 2
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 187 20 25 30
 190 Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
 191 35 40 45
 194 Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 195 50 55 60
 198 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 199 65 70 75 80
 202 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 203 85 90 95
 206 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 207 100 105 110
 210 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 211 115 120 125
 214 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 215 130 135 140
 218 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 219 145 150 155 160
 222 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 223 165 170 175
 226 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 227 180 185 190
 230 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
 231 195 200 205
 234 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 235 210 215 220
 238 Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 239 225 230 235 240
 242 Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
 243 245 250 255
 246 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 247 260 265 270
 250 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 251 275 280 285
 254 Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 255 290 295 300
 258 Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
 259 305 310 315 320
 262 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro

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270	Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg
271						355			360				365			
274	Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Leu	Ser	Val	Leu	Asp	
275						370			375				380			
278	Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val
279						385			390			395			400	
282	Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln
283						405				410				415		
286	Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His
287						420			425				430			
290	Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
291						435			440				445			
294	Arg	Ala	Pro	Thr	Phe	Ser	Trp	Gln	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
295						450			455				460			
298	Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
299						465			470			475			480	
302	Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
303						485			490				495			
306	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
307						500			505				510			
310	Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
311						515			520				525			
314	Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
315						530			535				540			
318	Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
319						545			550			555			560	
322	Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
323						565			570				575			
326	Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
327						580			585				590			
330	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
331						595			600				605			
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335						610			615				620			
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339						625			630			635			640	
342	Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
343						645			650				655			
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347						660			665				670			
350	His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
351						675			680				685			
354	Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
355						690			695				700			
358	Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
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362 Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
 363 725 730 735
 366 Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
 367 740 745 750
 370 Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
 371 755 760 765
 374 Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
 375 770 775 780
 378 Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
 379 785 790 795 800
 382 Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
 383 805 810 815
 386 Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
 387 820 825 830
 390 Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
 391 835 840 845
 394 Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
 395 850 855 860
 398 Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
 399 865 870 875 880
 402 Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
 403 885 890 895
 406 Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
 407 900 905 910
 410 Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
 411 915 920 925
 414 Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
 415 930 935 940
 418 Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
 419 945 950 955 960
 422 Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
 423 965 970 975
 426 Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
 427 980 985 990
 430 Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
 431 995 1000 1005
 434 Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
 435 1010 1015 1020
 438 Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
 439 1025 1030 1035
 442 Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
 443 1040 1045 1050
 446 Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
 447 1055 1060 1065
 450 Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
 451 1070 1075 1080
 454 Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
 455 1085 1090 1095
 458 Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys

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